WHAT IS CLAIMED IS:

1. A method for determining whether or not a continued arbitrary DNA sequence existing in the genome of an arbitrary biological species is the specific region, wherein said nucleotide sequence is known but its possibility of being a gene expression region is unclear (specific region), which comprises:

detecting whether or not a nucleotide sequence that corresponds to the nucleotide sequence of said region is present in the RNA of said biological species.

2. The method according to claim 1, wherein said specific region is a DNA region of from 100 to 200 bases.

3. The method according to claim 1 or 2, wherein said detection comprises detecting whether or not DNA or RNA is amplified by carrying out amplification of DNA or RNA based on the RNA of said biological species, using an oligonucleotide homologous to a sequence which is comprised of at least 10 or more continued bases and positioned in the 5′-end of said specific region and another oligonucleotide complementary to a sequence which is comprised of at least 10 or more continued bases and positioned in the 3′-end of said specific region.

4. The method according to claim 3, wherein at least one of said oligonucleotides has an RNA-transcriptable promoter sequence in its 5′-end and

said amplification is an RNA amplification comprising:

(1) synthesizing a DNA fragment complementary to a part of RNA of said biological species by RNA-dependent DNA polymerase from said either one of the oligonucleotides using said biological species-derived RNA as the template, thereby effecting formation of an RNA-DNA hybrid,

(2) forming a single-stranded DNA fragment by hydrolyzing the biological species-derived RNA of said RNA-DNA hybrid with ribonuclease H,

(3) synthesizing a DNA fragment complementary to said single-stranded DNA fragment by DNA-dependent DNA polymerase from the other oligonucleotide using the single-stranded DNA fragment as the template, thereby effecting formation of a double-stranded DNA fragment having a promoter sequence capable of performing transcription of RNA as a part of the RNA of said biological species or RNA complementary to a part thereof,

(4) forming an RNA transcription product from said double-stranded DNA using RNA polymerase, and

(5) the repeating the steps of from (1) to (4) using said RNA transcription product as the template.

5. The method according to claim 3 or 4, wherein said detection of whether or not DNA or RNA is amplified is carried out by a method comprising:

carrying out the amplification in the presence of an oligonucleotide probe which can specifically bind to the

DNA or RNA formed by the amplification and is labeled with an intercalating fluorescence dye, provided that said oligonucleotide is a sequence which does not form complementary bonding with any one of the aforementioned oligonucleotides, and

measuring the change in a fluorescence characteristic of the reaction solution.

6. The detection method according to claim 5, wherein said probe is capable of performing complementary binding with at least a part of the sequence of the DNA transcription product or RNA transcription product formed by the amplification to change the fluorescence characteristic as compared with the case in which the complex is not formed.

7. A method for determining the gene expression region in an arbitrary region on a genome or the entire genome, which comprises repeatedly carrying out the method of any one of claims 1 to 6.

8. A genomic gene which was determined to be a gene expression region by the method of any one of claims 1 to 7.

9. A protein encoded by the gene of claim 8.